

DB 23 YDIGELSGGQFAIVKCKEKGSTGLEVAKFKKRSRSGVSEEEEREVSILROYL 82
QY 61 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 120
DB 83 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 142
QY 121 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 180
DB 143 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 202
QY 181 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 240
DB 203 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 262
QY 241 RRLVETRRKRLTIOEALRHPWI 263
DB 263 RRLVETRRKRLTIOEALRHPWI 285

SULT 2

UIK4

PRELIMINARY:

PRT: A 370 AA.

AC O9UYK4
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99303018; PubMed-10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity".
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018001; BAA88063.1.
DR HSSP: Q63450; IAO6.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser-thr-kinase.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; STKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42898 MW; 035E914BDC881A2 CRC64.

Query Match 98.4%; Score 1321; DB 4; Length 370;
Best Local Similarity 98.9%; Pred. No. 1.1e-94;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YDIGELSGGQFAIVKCKEKGSTGLEVAKFKKRSRSGVSEEEEREVSILROYL 60
DB 23 YDIGELSGGQFAIVKCKEKGSTGLEVAKFKKRSRSGVSEEEEREVSILROYL 82
QY 61 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 120
DB 83 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 142
QY 121 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 180
DB 143 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 202

QY 181 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 240
DB 203 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 262
QY 241 RRLVETRRKRLTIOEALRHPWI 263
DB 263 RRLVETRRKRLTIOEALRHPWI 285

RESULT 3

O9UYM4

PRELIMINARY:

PRT: A 370 AA.

AC O9UYM4
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2 OR DAPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99303018; PubMed-10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity".
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018002; BAA88064.1.
DR HSSP: Q63450; IAO6.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser-thr-kinase.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; STKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42769 MW; 7DA6E29C4E6615B3 CRC64.

Query Match 96.6%; Score 1297; DB 11; Length 370;
Best Local Similarity 97.3%; Pred. No. 7.7e-93;
Matches 256; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 YDIGELSGGQFAIVKCKEKGSTGLEVAKFKKRSRSGVSEEEEREVSILROYL 60
DB 23 YDIGELSGGQFAIVKCKEKGSTGLEVAKFKKRSRSGVSEEEEREVSILROYL 82
QY 61 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 120
DB 83 HHNVITLHDVYENRDTDVVHILEVSGGELFDFLAOKESISEEATSFIKQIIDGVNYLHT 142
QY 121 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 180
DB 143 KRIAHFDLKPENIMLDKNIPPIPHIKLIDFGLAHEIEDGVEERKNIFGPEFVAPETIVN 202
QY 181 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 240
DB 203 PLGLADAMWSIGVITYILLSGASPLGDTKQETLANITSVSYDPDEEFSHTSELAADPI 262
QY 241 RRLVETRRKRLTIOEALRHPWI 263
DB 263 RRLVETRRKRLTIOEALRHPWI 285